

Thu May 27 15:15:47 2004

us-09-666-267b-8.rapb

Page: 2

ISSUE: 8
PAGES: 2714 TO 2722
DATE: 1989-10-15
DATABASE ACCESSION NUMBER: AAA36045
DATABASE ENTRY DATE: 1993-07-26
RELEVANT RESIDUES: (1)..(216)
US-10-339-876A-8

Query Match 100.0%; Score 1149; DB 15; Length 216;
Best Local Similarity 100.0%; Pred. No. 7.1e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVHYVTEKVEVATLSGHNVSVELAQTIRIYQKEXKMTLTMGSDNMTWPE 60
DB 1 GLSHFCGVHYVTEKVEVATLSGHNVSVELAQTIRIYQKEXKMTLTMGSDNMTWPE 60
QY 61 YKNTTIPITNNLSIVIALRPSDEGTVECVLKYEKDAFRRHLAEVTLVSKADPTPS 120
DB 61 YKNTTIPITNNLSIVIALRPSDEGTVECVLKYEKDAFRRHLAEVTLVSKADPTPS 120
QY 121 ISDEIPTSNIRRIICSTGGFPEPHLSWLENGSELNAINTTVSQDEPTELAVSSKLP 180
DB 121 ISDEIPTSNIRRIICSTGGFPEPHLSWLENGSELNAINTTVSQDEPTELAVSSKLP 180
QY 181 NMTNHSFMCILIKYGHLRVNOTFNMNTTKOEHPPDN 216
DB 181 NMTNHSFMCILIKYGHLRVNOTFNMNTTKOEHPPDN 216

RESULT 2
US-09-915-789A-21
Sequence 21, Application US/09915789A
Patent No. US20020168762A1
GENERAL INFORMATION:
APPLICANT: Chen, Lieping
TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
FILE REFERENCE: 07039-219001
CURRENT APPLICATION NUMBER: US/09/915,789A
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/220,991
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match 100.0%; Score 1149; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.5e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVHYVTEKVEVATLSGHNVSVELAQTIRIYQKEXKMTLTMGSDNMTWPE 60
DB 1 GLSHFCGVHYVTEKVEVATLSGHNVSVELAQTIRIYQKEXKMTLTMGSDNMTWPE 70
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DB 131 ISDEIPTSNIRRIICSTGGFPEPHLSWLENGSELNAINTTVSQDEPTELAVSSKLP 190
QY 181 NMTNHSFMCILIKYGHLRVNOTFNMNTTKOEHPPDN 216
DB 191 NMTNHSFMCILIKYGHLRVNOTFNMNTTKOEHPPDN 226

RESULT 3
US-08-592-711-2

Sequence 2, Application US/08592711
Publication No. US20020115214A1
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary U.
APPLICANT: Gray, Gary S.
APPLICANT: Renner, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCES/DOCKET NUMBER: RPT-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 15:13:49 ; Search time 46 Seconds
(without alignments)
1311.258 Million cell updates/sec

Title: US-09-666-267b-8

Perfect score: 1149
Sequence: 1 GLSHFGSGVHTVTKVEVA.....LRVNOTPNMTTKQHHFDPN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1149	100.0	288	US-09-772-102-14	Sequence 14, Appl1
5	1149	100.0	288	US-09-837-867A-19	Sequence 19, Appl1
6	1149	100.0	288	US-09-896-738-10	Sequence 10, Appl1
7	1149	100.0	288	US-09-915-789A-15	Sequence 15, Appl1
8	1149	100.0	288	US-09-966-969-19	Sequence 19, Appl1
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13	1149	100.0	288	US-10-261-101-2	GENERAL INFORMA
14	1149	100.0	288	US-10-032-214-278	Sequence 278, App

15	1149	100.0	288	US-10-126-088-2	Sequence 2, Appl1
17	1149	100.0	288	US-10-041-319-7	Sequence 7, Appl1
18	1149	100.0	288	US-10-330-330-2	Sequence 2, Appl1
19	1149	100.0	473	US-09-910-059-131	Sequence 131, Appl1
20	1149	99.5	9	US-09-845-895A-3	Sequence 3, Appl1
21	1129	98.3	288	US-10-032-214-64	Sequence 64, Appl1
22	1121	97.6	288	US-10-032-214-69	Sequence 69, Appl1
23	1121	97.6	288	US-10-032-214-82	Sequence 82, Appl1
24	1119	97.4	288	US-10-032-214-71	Sequence 71, Appl1
25	1119	97.4	288	US-10-032-214-77	Sequence 77, Appl1
26	1119	97.4	288	US-10-032-214-84	Sequence 84, Appl1
27	1118	97.3	288	US-10-032-214-84	Sequence 84, Appl1
28	1116	97.1	288	US-10-032-214-86	Sequence 86, Appl1
29	1116	97.1	288	US-10-032-214-87	Sequence 87, Appl1
30	1116	97.1	288	US-10-032-214-87	Sequence 87, Appl1
31	1116	97.1	288	US-10-032-214-86	Sequence 86, Appl1
32	1114	97.0	288	US-10-032-214-226	Sequence 226, App
33	1114	97.0	288	US-10-032-214-251	Sequence 251, App
34	1113	96.9	288	US-10-032-214-90	Sequence 90, Appl1
35	1113	96.9	288	US-10-032-214-228	Sequence 228, App
36	1113	96.9	288	US-10-032-214-250	Sequence 250, App
37	1112	96.8	288	US-10-032-214-78	Sequence 78, Appl1
38	1112	96.8	288	US-10-032-214-248	Sequence 248, App
39	1111	96.7	288	US-10-032-214-238	Sequence 238, App
40	1110	96.6	288	US-10-032-214-236	Sequence 236, App
41	1109	96.5	288	US-10-032-214-88	Sequence 88, Appl1
42	1109	96.5	288	US-10-032-214-89	Sequence 89, Appl1
43	1109	96.5	288	US-10-032-214-92	Sequence 92, Appl1
44	1109	96.5	288	US-10-032-214-249	Sequence 249, App
45	1108	96.4	287	US-10-032-214-243	Sequence 243, App

ALIGNMENTS

RESULT 1
US-10-339-876A-8
Sequence 8, Application US/10339876A
Publication No. US20030219446A1
GENERAL INFORMATION:
APPLICANT: Brady, William
APPLICANT: Lindsey, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damlie, Nilton K.
TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
FILE REFERENCE: 30436.11US07
CURRENT APPLICATION NUMBER: US/10/339,876A
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 07/498,949
PRIOR FILING DATE: 1990-03-26
PRIOR APPLICATION NUMBER: 07/547,980
PRIOR FILING DATE: 1990-07-02
PRIOR APPLICATION NUMBER: 07/722,101
PRIOR FILING DATE: 1991-06-27
PRIOR APPLICATION NUMBER: 08/219,200
PRIOR FILING DATE: 1994-03-29
PRIOR APPLICATION NUMBER: 08/459,766
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 09/569,164
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ. ID NOS: 8
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 216
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Gordon J. Freeman, Arnold S. Freeman, Jeffrey M. Segall, Grace
AUTHORS: Lee, James F. Whitman and Lee M. Nadler
TITLE: B7, A NEW MEMBER OF THE IG SUPERFAMILY WITH UNIQUE EXPRESSION ON
TITLE: ACTIVATED AND NEOPLASTIC B CELLS
JOURNAL: J. Immunol.
VOLUME: 143

Thu May 27 15:15:39 2004

us-09-666-267b-8.ra1

Page 1

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OM protein - protein search, using sw model

Run on: May 27, 2004, 15:12:55 ; Search time 22 Seconds

(without alignments)
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Title: US-09-666-267B-8

Perfect score: 1149
Sequence: 1 GLSHRCGSHVHTKKEVA.....LRVNTFNWTTKQHPEDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 385414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1149	100.0	288	2	US-08-101-624-23
4	1149	100.0	288	3	US-08-751-767A-6
5	1149	100.0	288	3	US-08-153-262-2
6	1149	100.0	288	3	US-08-478-744A-29
7	1149	100.0	288	3	US-08-280-757B-29
8	1149	100.0	288	3	US-09-159-135-2
9	1149	100.0	288	3	US-08-702-525-19
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12	1149	100.0	288	4	US-08-403-253A-2
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17	1149	100.0	288	4	US-09-837-867A-19
18	1149	100.0	288	4	US-09-910-174B-5
19	1149	100.0	288	4	US-09-620-461-5
20	1149	100.0	288	4	US-08-453-386A-2
21	1149	100.0	288	4	PCT-US95-02576-17
22	1149	100.0	473	3	US-09-171-945-131
23	1102	95.9	208	4	US-09-460-384-36
24	1100	95.7	288	4	US-09-651-200-14
25	1050	91.4	208	3	US-08-630-172-15
26	1050	91.4	208	3	US-09-375-419-15
27	743	64.7	292	4	US-09-651-200-16

28	743	64.7	292	4	US-09-303-040-2	Sequence 2, Appl1
29	739	64.3	292	4	US-09-303-040-4	Sequence 4, Appl1
30	738	64.2	299	4	US-09-651-200-15	Sequence 15, Appl1
31	561	48.8	306	3	US-08-205-697A-17	Sequence 17, Appl1
32	561	48.8	306	3	US-08-702-525-17	Sequence 17, Appl1
33	561	48.8	306	4	US-09-651-200-17	Sequence 17, Appl1
34	561	48.8	306	4	US-09-651-200-17	Sequence 17, Appl1
35	561	48.8	306	4	US-09-651-200-17	Sequence 17, Appl1
36	561	48.8	306	5	PCT-US95-02576-17	Sequence 17, Appl1
37	561	48.8	306	5	PCT-US95-02576-17	Sequence 17, Appl1
38	561	48.8	306	3	US-08-205-697A-2	Sequence 2, Appl1
39	561	48.8	320	3	US-08-702-525-2	Sequence 2, Appl1
40	561	48.8	320	4	US-09-637-867A-2	Sequence 2, Appl1
41	558	48.6	306	5	PCT-US95-02576-2	Sequence 2, Appl1
42	558	48.6	306	2	US-08-147-772-4	Sequence 4, Appl1
43	558	48.6	306	2	US-08-456-104-8	Sequence 8, Appl1
44	558	48.6	306	2	US-08-101-624-25	Sequence 25, Appl1
45	558	48.6	306	3	US-08-153-262-4	Sequence 4, Appl1
					US-08-479-744A-31	Sequence 31, Appl1

ALIGNMENTS

RESULT 1
US-08-147-772-2
Sequence 2, Application US/08147772
Patent No. 5858776
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragora, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RFI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE: for CD28 T cell surface antigen; transmembrane protein
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
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FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
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LOCATION: 236 to 254
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LOCATION: 19 to 21
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LOCATION: 198 to 200
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IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7. A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2
Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 8, 2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 27 GSHFGSGVHTVKEKVEKATLSGHNVSVELAQTIRYQKEKRWLTNMGDMNIMPE 86
QY 61 YKNRTIPDITNNLSIVILALRPSDEGYECVLYKEKDAFREHLAETLSVKADPTTPS 120
DB 87 YKNRTIPDITNNLSIVILALRPSDEGYECVLYKEKDAFREHLAETLSVKADPTTPS 146
QY 121 ISDFRIPSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELIYAVSSKIDF 180
DB 147 ISDFRIPSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSODPETELIYAVSSKIDF 206
QY 181 NMTTHSFMCLIKYGHILRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTTHSFMCLIKYGHILRVNQTFFNNTTKQEHFPDN 242
RESULT 2
US-08-456-104-6
Sequence 6, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandagorae, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids